REMARKS

Claims 25-34 are now pending, with claim 25 being the sole independent claim.

Claims 11-24 have been canceled without prejudice to or disclaimer of the subject matter recited therein.

Claims 25-34 have been added; support for these added claims can be found at least in the claims as originally filed and throughout the specification. No new matter has been added.

The specification has been amended at two locations to remove reference to the following URL: www.ncbi.nlm.nih.gov/BLAST/.

RESPONSE TO RESTRICTION REQUIREMENT

In response to the Restriction Requirement in the Office Action mailed September 27, 2002, Applicants hereby elect, without traverse, **Group I** (Claims 11-15, 20-21, and 23-24, drawn to an isolated polynucleotide, vectors, and cells comprising the same and **invention m** (Claims 11-24, each in part, as the inventions pertains to SEQ ID NO:1 (nucleotide sequence of SEQ ID NO:1, which encodes the amino acid sequence of SEQ ID NO:2)).

Applicants believe that now pending claims 25-34 are directed to Group I.

Please charge any fees or credit any overpayment of fees which are required in connection herewith to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,

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Dated: 27 January 2003

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown within bolded brackets and stricken through, and inserted material is shown underlined.

IN THE SPECIFICATION:

At page 1, line 2:
SUCROSE TRANSPORT PROTEINS **[**~~SUCROSE TRANPORTERS~~**]**

Paragraph at page 5, line 34 through page 6, line 18:

A "substantial portion" of an amino acid or nucleotide sequence comprises enough of the amino acid sequence of a polypeptide or the nucleotide sequence of a gene to afford putative identification of that polypeptide or gene, either by manual evaluation of the sequence by one skilled in the art, or by computer-automated sequence comparison and identification using algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) *J. Mol. Biol. 215*:403-410**[**~~; see also www.ncbi.nlm.nih.gov/BLAST/~~**]**). In general, a sequence of ten or more contiguous amino acids or thirty or more nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene specific oligonucleotide probes comprising 20-30 contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12-15 bases may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises enough of the sequence to afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches partial or complete amino acid and nucleotide sequences encoding one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph at page 16, lines 6-23:

ESTs encoding sucrose transport proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) *J. Mol. Biol. 215*:403-410[~~; see also www.ncbi.nlm.nih.gov/BLAST/~~]) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. (1993) *Nature Genetics 3*:266-272 and Altschul, Stephen F., et al. (1997) *Nucleic Acids Res. 25*:3389-3402) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

At page 27, line 2:
SUCROSE TRANSPORT PROTEINS [~~SUCROSE TRANPORTERS~~]